

### FIG. 1A

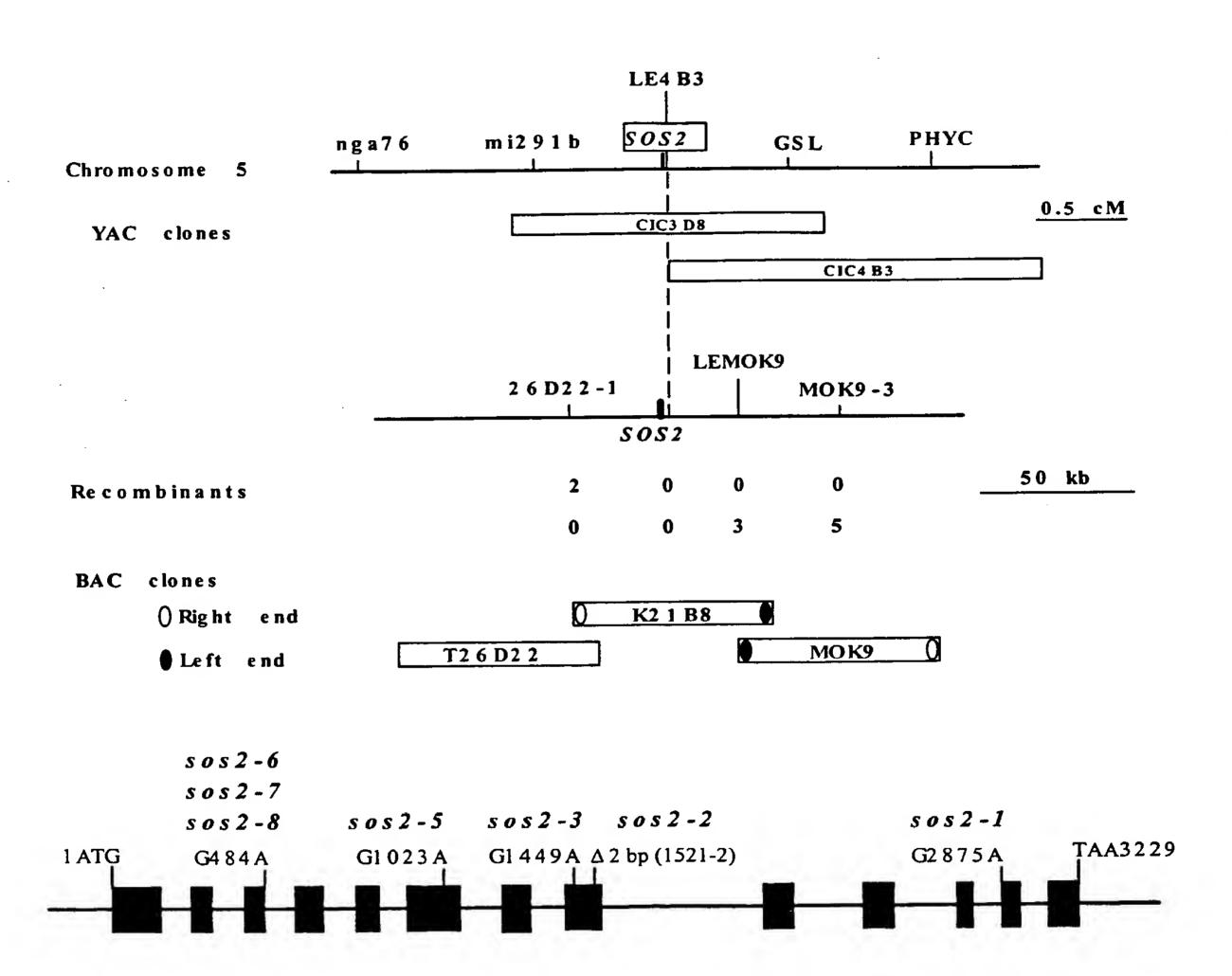
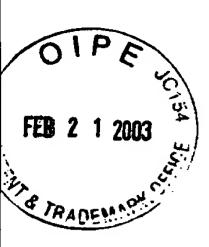


FIG. 1B



## FIG. 2A

Kinase Regulatory Domain

# FIG. 2B

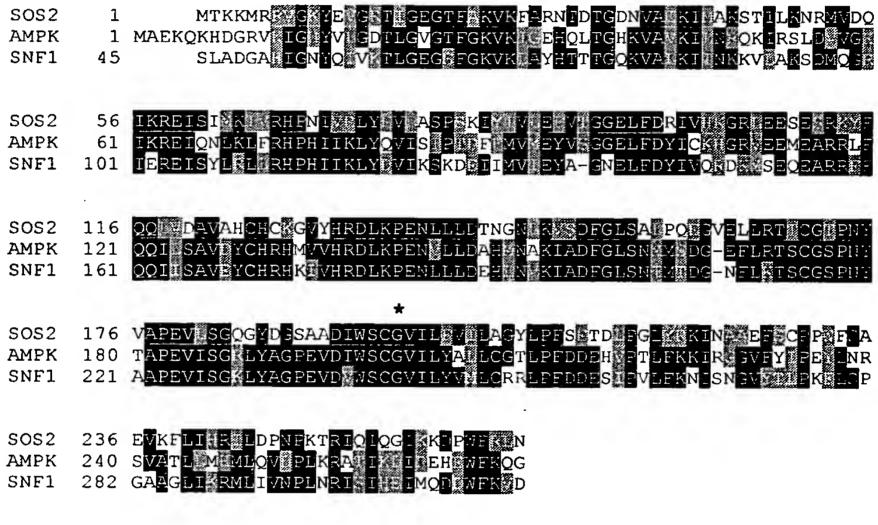
B																					_		_			
:																			TCC	ATC	:AGA	TAA	AAG	177	GIA	AAGA
1								AGT V											E		T					TAAG K
27								TCG G							I	M		TAA	YGAC	TAC	TAA:					AATG M
53				ì	ĸ	R		GAT.	S			GAA	GAT	TGI	$\tau \infty$	TCA			Ĭ.	V		Ļ	Y			GTO L
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105								TCG R						CCT	าต	ACA	TCC	TGI	A	Ĥ		Н	C			rgi i V
131								AGA E											rga/	KCCT	TTC	CCA			L	CAGT S
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209			TTC					TCC P					GAAA K	I I	AA. N	A	ACC									TTCC S
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261								-	-	a	TA	ΓAC		<b>.</b> AA(	M											ЛСС/ A
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339								_																		TAA( K
365									_																	AGA0
391									_	_																F
417																										CAG/ R

ACAATCACGITTTGATCCCAACTTAA

437 T I T F



### FIG. 3A



### FIG. 3B



SOS2 389 IE YE PSLF VLVRKAACETLE KF KK CSKLENIIWRATEGIT YCHK1 449 IELTN CHNLEL FIKRNGDPLE KFFKN VSS GKPIVLTDVSQN hCHK1 428 NILE D-DKILVDFPLSKGDGLE KHELK KGKLIDI SSQKW

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(Alassos)	
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FIG. 4



